



SEQUENCE LISTING

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(1) GENERAL INFORMATION:

- 5 (i) APPLICANT: Lester, Henry A.
Davidson, Norman
Kofuji, Paulo
- 10 (ii) TITLE OF INVENTION: INWARD RECTIFIER, G-PROTEIN ACTIVATED,
MAMMALIAN, POTASSIUM CHANNELS AND USES THEREOF
- (iii) NUMBER OF SEQUENCES: 6
- 15 (iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: Flehr Hohbach Test Albritton & Herbert LLP
(B) STREET: Four Embarcadero Center, Suite 3400
(C) CITY: San Francisco
(D) STATE: California
20 (E) COUNTRY: United States
(F) ZIP: 94111-4187
- (v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
25 (B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
30 (A) APPLICATION NUMBER: US 09/039,927
(B) FILING DATE: 16-MAR-1998
(C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
35 (A) APPLICATION NUMBER: US 08/066,371
(B) FILING DATE: 21-MAR-1993
- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: US 08/614,801
40 (B) FILING DATE: 07-MAR-1996
- (viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: Trecartin, Richard F.
(B) REGISTRATION NUMBER: 31,801
45 (C) REFERENCE/DOCKET NUMBER: A-63098-1/RFT
- (ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: (415) 781-1989
(B) TELEFAX: (415) 398-3249
50 (C) TELEX: 910 277299
- (2) INFORMATION FOR SEQ ID NO:1:
- (i) SEQUENCE CHARACTERISTICS:
55 (A) LENGTH: 2070 base pairs
(B) TYPE: nucleic acid

(C) STRANDEDNESS: unknown

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 32..1534

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GGCACGAGAA TCTGGATCTC CCCTCCGTAT T ATG TCT GCA CTC CGA AGG AAA 52
Met Ser Ala Leu Arg Arg Lys
1 5

TTT GGG GAC GAT TAC CAG GTA GTG ACC ACT TCG TCC AGC GGT TCG GGC 100
Phe Gly Asp Asp Tyr Gln Val Val Thr Thr Ser Ser Ser Gly Ser Gly
10 15 20

TTG CAG CCC CAG GGG CCA GGA CAG GGC CCA CAG CAG CAG CTT GTA CCC 148
Leu Gln Pro Gln Gly Pro Gly Gln Gly Pro Gln Gln Gln Leu Val Pro
25 30 35

AAG AAG AAA CGG CAG CGG TTC GTG GAC AAG AAC GGT CGG TGC AAT GTG 196
Lys Lys Lys Arg Gln Arg Phe Val Asp Lys Asn Gly Arg Cys Asn Val
40 45 50 55

CAG CAC GGC AAC CTG GGC AGC GAG ACC AGT CGC TAC CTT TCC GAC CTC 244
Gln His Gly Asn Leu Gly Ser Glu Thr Ser Arg Tyr Leu Ser Asp Leu
60 65 70

TTC ACT ACC CTG GTG GAT CTC AAG TGG CGT TGG AAC CTC TTT ATC TTC 292
Phe Thr Thr Leu Val Asp Leu Lys Trp Arg Trp Asn Leu Phe Ile Phe
75 80 85

ATC CTC ACC TAC ACC GTG GCC TGG CTC TTC ATG GCG TCC ATG TGG TGG 340
Ile Leu Thr Tyr Thr Val Ala Trp Leu Phe Met Ala Ser Met Trp Trp
90 95 100

GTG ATC GCT TAT ACC CGG GGC GAC CTG AAC AAA GCC CAT GTC GGC AAC 388
Val Ile Ala Tyr Thr Arg Gly Asp Leu Asn Lys Ala His Val Gly Asn
105 110 115

TAC ACT CCC TGT GTG GCC AAT GTC TAT AAC TTC CCC TCT GCC TTC CTT 436
Tyr Thr Pro Cys Val Ala Asn Val Tyr Asn Phe Pro Ser Ala Phe Leu
120 125 130 135

TTC TTC ATC GAG ACC GAG GCC ACC ATC GGC TAT GGC TAC CGC TAC ATC 484
Phe Phe Ile Glu Thr Glu Ala Thr Ile Gly Tyr Gly Tyr Arg Tyr Ile
140 145 150

ACC GAC AAG TGC CCC GAG GGC ATC ATC CTT TTC CTT TTC CAG TCC ATC 532
Thr Asp Lys Cys Pro Glu Gly Ile Ile Leu Phe Leu Phe Gln Ser Ile
155 160 165

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	CTT GGC TCC ATC GTG GAC GCT TTC CTC ATC GGC TGC ATG TTC ATC AAG	580
	Leu Gly Ser Ile Val Asp Ala Phe Leu Ile Gly Cys Met Phe Ile Lys	
	170 175 180	
5	ATG TCC CAG CCC AAA AAG CGC GCC GAG ACC CTC ATG TTT AGC GAG CAT	628
	Met Ser Gln Pro Lys Lys Arg Ala Glu Thr Leu Met Phe Ser Glu His	
	185 190 195	
10	GCG GTT ATT TCC ATG AGG GAC GGA AAA CTC ACT CTC ATG TTC CGG GTG	676
	Ala Val Ile Ser Met Arg Asp Gly Lys Leu Thr Leu Met Phe Arg Val	
	200 205 210 215	
15	GGC AAC CTG CGC AAC AGC CAC ATG GTC TCC GCG CAG ATC CGC TGC AAG	724
	Gly Asn Leu Arg Asn Ser His Met Val Ser Ala Gln Ile Arg Cys Lys	
	220 225 230	
20	CTG CTC AAA TCT CGG CAG ACA CCT GAG GGT GAG TTT CTA CCC CTT GAC	772
	Leu Leu Lys Ser Arg Gln Thr Pro Glu Gly Glu Phe Leu Pro Leu Asp	
	235 240 245	
25	CAA CTT GAA CTG GAT GTA GGT TTT AGT ACA GGG GCA GAT CAA CTT TTT	820
	Gln Leu Glu Leu Asp Val Gly Phe Ser Thr Gly Ala Asp Gln Leu Phe	
	250 255 260	
30	CTT GTG TCC CCT CTC ACC ATT TGC CAC GTG ATC GAT GCC AAA AGC CCC	868
	Leu Val Ser Pro Leu Thr Ile Cys His Val Ile Asp Ala Lys Ser Pro	
	265 270 275	
35	TTT TAT GAC CTA TCC CAG CGA AGC ATG CAA ACT GAA CAG TTC GAG GTG	916
	Phe Tyr Asp Leu Ser Gln Arg Ser Met Gln Thr Glu Gln Phe Glu Val	
	280 285 290 295	
40	GTC GTC ATC CTG GAA GGC ATC GTG GAA ACC ACA GGG ATG ACT TGT CAA	964
	Val Val Ile Leu Glu Gly Ile Val Glu Thr Thr Gly Met Thr Cys Gln	
	300 305 310	
45	GCT CGA ACA TCA TAC ACC GAA GAT GAA GTT CTT TGG GGT CAT CGT TTT	1012
	Ala Arg Thr Ser Tyr Thr Glu Asp Glu Val Leu Trp Gly His Arg Phe	
	315 320 325	
50	TTC CCT GTA ATT TCT TTA GAA GAA GGA TTC TTT AAA GTC GAT TAC TCC	1060
	Phe Pro Val Ile Ser Leu Glu Glu Gly Phe Phe Lys Val Asp Tyr Ser	
	330 335 340	
55	CAG TTC CAT GCA ACC TTT GAA GTC CCC ACC CCT CCG TAC AGT GTG AAA	1108
	Gln Phe His Ala Thr Phe Glu Val Pro Thr Pro Pro Tyr Ser Val Lys	
	345 350 355	
60	GAG CAG GAA GAA ATG CTT CTC ATG TCT TCC CCT TTA ATA GCA CCA GCC	1156
	Glu Gln Glu Glu Met Leu Leu Met Ser Ser Pro Leu Ile Ala Pro Ala	
	360 365 370 375	
65	ATA ACC AAC AGC AAA GAA AGA CAC AAT TCT GTG GAG TGC TTA GAT GGA	1204
	Ile Thr Asn Ser Lys Glu Arg His Asn Ser Val Glu Cys Leu Asp Gly	
	380 385 390	

	CTA GAT GAC ATT AGC ACA AAA CTT CCA TCG AAG CTG CAG AAA ATT ACG	1252
	Leu Asp Asp Ile Ser Thr Lys Leu Pro Ser Lys Leu Gln Lys Ile Thr	
	395 400 405	
5	GGG AGA GAA GAC TTT CCC AAA AAA CTC CTG AGG ATG AGT TCT ACA ACT	1300
	Gly Arg Glu Asp Phe Pro Lys Lys Leu Leu Arg Met Ser Ser Thr Thr	
	410 415 420	
10	TCA GAA AAA GCC TAT AGT TTG GGT GAT TTG CCC ATG AAA CTC CAA CGA	1348
	Ser Glu Lys Ala Tyr Ser Leu Gly Asp Leu Pro Met Lys Leu Gln Arg	
	425 430 435	
15	ATA AGT TCG GTT CCT GGC AAC TCT GAA GAA AAA CTG GTA TCT AAA ACC	1396
	Ile Ser Ser Val Pro Gly Asn Ser Glu Glu Lys Leu Val Ser Lys Thr	
	440 445 450 455	
20	ACC AAG ATG TTA TCA GAT CCC ATG AGC CAG TCT GTG GCC GAT TTG CCA	1444
	Thr Lys Met Leu Ser Asp Pro Met Ser Gln Ser Val Ala Asp Leu Pro	
	460 465 470	
25	CCG AAG CTT CAA AAG ATG GCT GGA GGA CCT ACC AGG ATG GAA GGG AAT	1492
	Pro Lys Leu Gln Lys Met Ala Gly Gly Pro Thr Arg Met Glu Gly Asn	
	475 480 485	
30	CTT CCA GCC AAA CTA AGA AAA ATG AAC TCT GAC CGC TTC ACA	1534
	Leu Pro Ala Lys Leu Arg Lys Met Asn Ser Asp Arg Phe Thr	
	490 495 500	
35	TAGCAAAACA CCCCATTAGG CATTATTTCA TGTTTTGATT TAGTTTTAGT CCAATATTTG	1594
	GCTGATAAGA TAATCCTCCC CGGGAAATCT GAGAGGTCTA TCCCAGTCTG GCAAATTCAT	1654
	CAGAGGACTC TTCATTGAAG TGTTGTTACT GTGTTGAACA TGAGTTACAA AGGGAGGACA	1714
40	TCATAAGAAA GCTAATAGTT GGCATGTATT ATCACATCAA GCATGCAATA ATGTGCAAAT	1774
	TTTGCATTTA GTTTTCTGGC ATGATTTATA TATGGCATAT TTATATTGAA TATTCTGGAA	1834
	AAATATATAA ATATATATTT GAAGTGGAGA TATTCTCCCC ATAATTTCTA ATATATGTAT	1894
45	TAAGCCAAAC ATGAGTGGAT AGCTTTCAGG GCACTAAAT AATATACATG CATAACATACA	1954
	TACATGCATA TGCACAGACA CATAACACACA CATACTCATA TATATAAAAC ATACCCATAC	2014
	AAACATATAT ATCTAATAAA AATTGTGATG TTTTGTTCOA AAAAAAAAAA AAAAAA	2070

(2) INFORMATION FOR SEQ ID NO:2:

- 50 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 501 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- 55 (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

	Met	Ser	Ala	Leu	Arg	Arg	Lys	Phe	Gly	Asp	Asp	Tyr	Gln	Val	Val	Thr	
	1				5					10					15		
5	Thr	Ser	Ser	Ser	Gly	Ser	Gly	Leu	Gln	Pro	Gln	Gly	Pro	Gly	Gln	Gly	
				20					25					30			
	Pro	Gln	Gln	Gln	Leu	Val	Pro	Lys	Lys	Lys	Arg	Gln	Arg	Phe	Val	Asp	
10			35					40					45				
	Lys	Asn	Gly	Arg	Cys	Asn	Val	Gln	His	Gly	Asn	Leu	Gly	Ser	Glu	Thr	
		50					55					60					
15	Ser	Arg	Tyr	Leu	Ser	Asp	Leu	Phe	Thr	Thr	Leu	Val	Asp	Leu	Lys	Trp	
	65					70					75					80	
	Arg	Trp	Asn	Leu	Phe	Ile	Phe	Ile	Leu	Thr	Tyr	Thr	Val	Ala	Trp	Leu	
					85					90					95		
20	Phe	Met	Ala	Ser	Met	Trp	Trp	Val	Ile	Ala	Tyr	Thr	Arg	Gly	Asp	Leu	
				100					105					110			
	Asn	Lys	Ala	His	Val	Gly	Asn	Tyr	Thr	Pro	Cys	Val	Ala	Asn	Val	Tyr	
25			115					120					125				
	Asn	Phe	Pro	Ser	Ala	Phe	Leu	Phe	Phe	Ile	Glu	Thr	Glu	Ala	Thr	Ile	
		130					135					140					
30	Gly	Tyr	Gly	Tyr	Arg	Tyr	Ile	Thr	Asp	Lys	Cys	Pro	Glu	Gly	Ile	Ile	
	145					150					155					160	
	Leu	Phe	Leu	Phe	Gln	Ser	Ile	Leu	Gly	Ser	Ile	Val	Asp	Ala	Phe	Leu	
					165					170					175		
35	Ile	Gly	Cys	Met	Phe	Ile	Lys	Met	Ser	Gln	Pro	Lys	Lys	Arg	Ala	Glu	
				180					185					190			
	Thr	Leu	Met	Phe	Ser	Glu	His	Ala	Val	Ile	Ser	Met	Arg	Asp	Gly	Lys	
40			195					200					205				
	Leu	Thr	Leu	Met	Phe	Arg	Val	Gly	Asn	Leu	Arg	Asn	Ser	His	Met	Val	
		210					215					220					
45	Ser	Ala	Gln	Ile	Arg	Cys	Lys	Leu	Leu	Lys	Ser	Arg	Gln	Thr	Pro	Glu	
	225					230				235						240	
	Gly	Glu	Phe	Leu	Pro	Leu	Asp	Gln	Leu	Glu	Leu	Asp	Val	Gly	Phe	Ser	
					245					250					255		
50	Thr	Gly	Ala	Asp	Gln	Leu	Phe	Leu	Val	Ser	Pro	Leu	Thr	Ile	Cys	His	
				260					265					270			
	Val	Ile	Asp	Ala	Lys	Ser	Pro	Phe	Tyr	Asp	Leu	Ser	Gln	Arg	Ser	Met	
55			275					280					285				

Gln Thr Glu Gln Phe Glu Val Val Val Ile Leu Glu Gly Ile Val Glu
 290 295 300
 Thr Thr Gly Met Thr Cys Gln Ala Arg Thr Ser Tyr Thr Glu Asp Glu
 5 305 310 315 320
 Val Leu Trp Gly His Arg Phe Phe Pro Val Ile Ser Leu Glu Glu Gly
 325 330 335
 10 Phe Phe Lys Val Asp Tyr Ser Gln Phe His Ala Thr Phe Glu Val Pro
 340 345 350
 Thr Pro Pro Tyr Ser Val Lys Glu Gln Glu Glu Met Leu Leu Met Ser
 355 360 365
 15 Ser Pro Leu Ile Ala Pro Ala Ile Thr Asn Ser Lys Glu Arg His Asn
 370 375 380
 Ser Val Glu Cys Leu Asp Gly Leu Asp Asp Ile Ser Thr Lys Leu Pro
 20 385 390 395 400
 Ser Lys Leu Gln Lys Ile Thr Gly Arg Glu Asp Phe Pro Lys Lys Leu
 405 410 415
 25 Leu Arg Met Ser Ser Thr Thr Ser Glu Lys Ala Tyr Ser Leu Gly Asp
 420 425 430
 Leu Pro Met Lys Leu Gln Arg Ile Ser Ser Val Pro Gly Asn Ser Glu
 435 440 445
 30 Glu Lys Leu Val Ser Lys Thr Thr Lys Met Leu Ser Asp Pro Met Ser
 450 455 460
 Gln Ser Val Ala Asp Leu Pro Pro Lys Leu Gln Lys Met Ala Gly Gly
 35 465 470 475 480
 Pro Thr Arg Met Glu Gly Asn Leu Pro Ala Lys Leu Arg Lys Met Asn
 485 490 495
 40 Ser Asp Arg Phe Thr
 500

(2) INFORMATION FOR SEQ ID NO:3:

- 45 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1978 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown
 50
 (ii) MOLECULE TYPE: DNA (genomic)
 (ix) FEATURE:
 (A) NAME/KEY: CDS
 55 (B) LOCATION: 488..1729

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

	GTCTCCCTGC AAGGTCTATC ACTTTGCTCC TAAACGAGGA TTTATTCCCT CTGCCACTCA	60
5	AGGCTGTCCC CCAGTTTCCT CGCAACCGGG CTTCCTCCTC AGTCCCCTGCC CACACGCGCA	120
	CTCCTCTGCC CCGCGGTGGC CCCAGCGCCC AGCCCTCCAG CCAGAGGGAG CCAGGCACCA	180
	GACGGCAGCA CCTGGCTGGA GAGGTTGGGC GGGCCGAGGG TGGGGATCCG CGGGAACCGG	240
10	CGAGTCGGAG CTGGAGCAGG AGCTGGACCC AACCGCTAGC AGCAGAATGG AGTCTCCTGA	300
	AAGCCTGCCG GGGCTGATGT GAAATTGGGC CATCTGCTTC CAGTTGGTCT GTTTCCTCCT	360
15	TTTCTTGAT TTTCTTCCCT CGCCATTAC CGTGGAGTGA ATTATTGAAT CTGCTCCGT	420
	TCCGAGAGAG GCGATCAGGA TGGAGTGAAC CTACCCTGTC CACTACAAGG AAAAGCACAA	480
20	AGAAGAA ATG ACA ATG GCC AAG TTA ACT GAA TCC ATG ACT AAC GTC TTG Met Thr Met Ala Lys Leu Thr Glu Ser Met Thr Asn Val Leu	529
	1 5 10	
	GAA GGC GAT TCC ATG GAC CAG GAT GTG GAA AGC CCA GTG GCC ATT CAC	577
25	Glu Gly Asp Ser Met Asp Gln Asp Val Glu Ser Pro Val Ala Ile His	
	15 20 25 30	
	CAG CCA AAG TTG CCT AAG CAG GCC AGG GAC GAC CTG CCG AGA CAC ATC	625
	Gln Pro Lys Leu Pro Lys Gln Ala Arg Asp Asp Leu Pro Arg His Ile	
30	35 40 45	
	AGC CGA GAC AGG ACC AAA AGG AAA ATC CAG AGG TAC GTG AGG AAG GAT	673
	Ser Arg Asp Arg Thr Lys Arg Lys Ile Gln Arg Tyr Val Arg Lys Asp	
	50 55 60	
35	GGG AAG TGC AAC GTT CAC CAC GGC AAT GTG CGG GAG ACC TAC CGA TAC	721
	Gly Lys Cys Asn Val His His Gly Asn Val Arg Glu Thr Tyr Arg Tyr	
	65 70 75	
	CTG ACG GAC ATC TTC ACC ACC CTG GTG GAC CTG AAG TGG AGA TTC AAC	769
40	Leu Thr Asp Ile Phe Thr Thr Leu Val Asp Leu Lys Trp Arg Phe Asn	
	80 85 90	
	CTG TTG ATC TTT GTC ATG GTC TAC ACA GTG ACG TGG CTT TTC TTT GGG	817
45	Leu Leu Ile Phe Val Met Val Tyr Thr Val Thr Trp Leu Phe Phe Gly	
	95 100 105 110	
	ATG ATC TGG TGG CTG ATT GCG TAC ATC CGG GGA GAT ATG GAC CAC ATA	865
	Met Ile Trp Trp Leu Ile Ala Tyr Ile Arg Gly Asp Met Asp His Ile	
50	115 120 125	
	GAG GAC CCC TCG TGG ACT CCT TGT GTC ACC AAC CTC AAC GGG TTT GTC	913
	Glu Asp Pro Ser Trp Thr Pro Cys Val Thr Asn Leu Asn Gly Phe Val	
	130 135 140	
55		

	TCT GCT TTT TTA TTC TCC ATA GAG ACA GAA ACC ACC ATC GGT TAT GGC	961
	Ser Ala Phe Leu Phe Ser Ile Glu Thr Glu Thr Thr Ile Gly Tyr Gly	
	145 150 155	
5	TAC CGG GTC ATC ACG GAC AAG TGC CCT GAG GGG ATT ATT CTC CTC TTA	1009
	Tyr Arg Val Ile Thr Asp Lys Cys Pro Glu Gly Ile Ile Leu Leu Leu	
	160 165 170	
10	ATC CAG TCC GTG TTG GGG TCC ATT GTC AAC GCC TTC ATG GTA GGA TGT	1057
	Ile Gln Ser Val Leu Gly Ser Ile Val Asn Ala Phe Met Val Gly Cys	
	175 180 185 190	
15	ATG TTT GTG AAA ATA TCC CAA CCC AAG AAG AGG GCA GAG ACC CTG GTC	1105
	Met Phe Val Lys Ile Ser Gln Pro Lys Lys Arg Ala Glu Thr Leu Val	
	195 200 205	
20	TTT TCC ACC CAC GCG GTG ATC TCC ATG CGG GAT GGG AAA CTG TGC TTG	1153
	Phe Ser Thr His Ala Val Ile Ser Met Arg Asp Gly Lys Leu Cys Leu	
	210 215 220	
25	ATG TTC CGG GTG GGG GAC TTG AGG AAT TCT CAC ATT GTG GAG GCA TCC	1201
	Met Phe Arg Val Gly Asp Leu Arg Asn Ser His Ile Val Glu Ala Ser	
	225 230 235	
30	ATC AGA GCC AAG TTG ATC AAG TCC AAA CAG ACT TCA GAG GGG GAG TTT	1249
	Ile Arg Ala Lys Leu Ile Lys Ser Lys Gln Thr Ser Glu Gly Glu Phe	
	240 245 250	
35	ATT CCC CTC AAC CAG AGT GAT ATC AAC GTG GGG TAC TAC ACA GGG GAC	1297
	Ile Pro Leu Asn Gln Ser Asp Ile Asn Val Gly Tyr Tyr Thr Gly Asp	
	255 260 265 270	
40	GAC CGG CTC TTT CTG GTG TCA CCA TTG ATT ATT AGC CAT GAA ATT AAC	1345
	Asp Arg Leu Phe Leu Val Ser Pro Leu Ile Ile Ser His Glu Ile Asn	
	275 280 285	
45	CAA CAG AGT CCC TTC TGG GAG ATC TCC AAA GCG CAG CTG CCT AAA GAG	1393
	Gln Gln Ser Pro Phe Trp Glu Ile Ser Lys Ala Gln Leu Pro Lys Glu	
	290 295 300	
50	GAA CTG GAG ATT GTG GTC ATC CTG GAG GGA ATC GTG GAA GCC ACA GGA	1441
	Glu Leu Glu Ile Val Val Ile Leu Glu Gly Ile Val Glu Ala Thr Gly	
	305 310 315	
55	ATG ACG TGC CAA GCC CGA AGC TCC TAC ATC ACC AGT GAG ATC TTG TGG	1489
	Met Thr Cys Gln Ala Arg Ser Ser Tyr Ile Thr Ser Glu Ile Leu Trp	
	320 325 330	
55	GGT TAC CGG TTC ACA CCT GTC CTA ACG ATG GAA GAC GGG TTC TAC GAA	1537
	Gly Tyr Arg Phe Thr Pro Val Leu Thr Met Glu Asp Gly Phe Tyr Glu	
	335 340 345 350	
55	GTT GAC TAC AAC AGC TTC CAT GAG ACC TAT GAG ACC AGC ACC CCG TCC	1585
	Val Asp Tyr Asn Ser Phe His Glu Thr Tyr Glu Thr Ser Thr Pro Ser	
	355 360 365	

CTT AGT GCC AAA GAG CTA GCG GAG CTG GCT AAC CGG GCA GAG GTG CCT 1633
 Leu Ser Ala Lys Glu Leu Ala Glu Leu Ala Asn Arg Ala Glu Val Pro
 370 375 380

5 CTG AGT TGG TCT GTG TCC AGC AAA CTG AAC CAA CAT GCA GAA TTG GAG 1681
 Leu Ser Trp Ser Val Ser Ser Lys Leu Asn Gln His Ala Glu Leu Glu
 385 390 395

10 ACA GAA GAG GAA GAG AAG AAC CCG GAA GAA CTG ACG GAG AGG AAT GGG 1729
 Thr Glu Glu Glu Glu Lys Asn Pro Glu Glu Leu Thr Glu Arg Asn Gly
 400 405 410

TGATGCTGGG CTCCTAGTGT GGATCAAGAA GTGTTCTTC TAAGCTCATC CTCTGACAGA 1789

15 CATTACAGAG AACTGATATA TTTTCCTCC TTTACTGCTT GGAAGAATTC ACCCAGAATT 1849

CACCCACCCC ATCTGGACCT AGTACATTCT GTTTGGGAAG GTCATCATT ATTTTACTTA 1909

AAGTCGGCGC TGGAGAGATG ACGCCGCGGG CTAAGATGGT TTATTGTTCT TGCAGACGGC 1969

20 CTGGGGTTCA 1978

(2) INFORMATION FOR SEQ ID NO:4:

25

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 414 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

30

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

35 Met Thr Met Ala Lys Leu Thr Glu Ser Met Thr Asn Val Leu Glu Gly
 1 5 10 15

Asp Ser Met Asp Gln Asp Val Glu Ser Pro Val Ala Ile His Gln Pro
 20 25 30

40 Lys Leu Pro Lys Gln Ala Arg Asp Asp Leu Pro Arg His Ile Ser Arg
 35 40 45

45 Asp Arg Thr Lys Arg Lys Ile Gln Arg Tyr Val Arg Lys Asp Gly Lys
 50 55 60

Cys Asn Val His His Gly Asn Val Arg Glu Thr Tyr Arg Tyr Leu Thr
 65 70 75 80

50 Asp Ile Phe Thr Thr Leu Val Asp Leu Lys Trp Arg Phe Asn Leu Leu
 85 90 95

Ile Phe Val Met Val Tyr Thr Val Thr Trp Leu Phe Phe Gly Met Ile
 100 105 110

55

	Trp	Trp	Leu	Ile	Ala	Tyr	Ile	Arg	Gly	Asp	Met	Asp	His	Ile	Glu	Asp	
			115					120					125				
5	Pro	Ser	Trp	Thr	Pro	Cys	Val	Thr	Asn	Leu	Asn	Gly	Phe	Val	Ser	Ala	
		130					135					140					
	Phe	Leu	Phe	Ser	Ile	Glu	Thr	Glu	Thr	Thr	Ile	Gly	Tyr	Gly	Tyr	Arg	
	145					150					155					160	
10	Val	Ile	Thr	Asp	Lys	Cys	Pro	Glu	Gly	Ile	Ile	Leu	Leu	Leu	Ile	Gln	
					165					170					175		
	Ser	Val	Leu	Gly	Ser	Ile	Val	Asn	Ala	Phe	Met	Val	Gly	Cys	Met	Phe	
				180					185					190			
15	Val	Lys	Ile	Ser	Gln	Pro	Lys	Lys	Arg	Ala	Glu	Thr	Leu	Val	Phe	Ser	
		195						200					205				
	Thr	His	Ala	Val	Ile	Ser	Met	Arg	Asp	Gly	Lys	Leu	Cys	Leu	Met	Phe	
20		210					215					220					
	Arg	Val	Gly	Asp	Leu	Arg	Asn	Ser	His	Ile	Val	Glu	Ala	Ser	Ile	Arg	
	225					230					235					240	
25	Ala	Lys	Leu	Ile	Lys	Ser	Lys	Gln	Thr	Ser	Glu	Gly	Glu	Phe	Ile	Pro	
					245					250					255		
	Leu	Asn	Gln	Ser	Asp	Ile	Asn	Val	Gly	Tyr	Tyr	Thr	Gly	Asp	Asp	Arg	
				260					265					270			
30	Leu	Phe	Leu	Val	Ser	Pro	Leu	Ile	Ile	Ser	His	Glu	Ile	Asn	Gln	Gln	
		275						280					285				
	Ser	Pro	Phe	Trp	Glu	Ile	Ser	Lys	Ala	Gln	Leu	Pro	Lys	Glu	Glu	Leu	
35		290					295					300					
	Glu	Ile	Val	Val	Ile	Leu	Glu	Gly	Ile	Val	Glu	Ala	Thr	Gly	Met	Thr	
	305					310				315						320	
40	Cys	Gln	Ala	Arg	Ser	Ser	Tyr	Ile	Thr	Ser	Glu	Ile	Leu	Trp	Gly	Tyr	
					325					330					335		
	Arg	Phe	Thr	Pro	Val	Leu	Thr	Met	Glu	Asp	Gly	Phe	Tyr	Glu	Val	Asp	
				340					345					350			
45	Tyr	Asn	Ser	Phe	His	Glu	Thr	Tyr	Glu	Thr	Ser	Thr	Pro	Ser	Leu	Ser	
		355						360					365				
	Ala	Lys	Glu	Leu	Ala	Glu	Leu	Ala	Asn	Arg	Ala	Glu	Val	Pro	Leu	Ser	
50		370					375					380					
	Trp	Ser	Val	Ser	Ser	Lys	Leu	Asn	Gln	His	Ala	Glu	Leu	Glu	Thr	Glu	
	385					390					395					400	
55	Glu	Glu	Glu	Lys	Asn	Pro	Glu	Glu	Leu	Thr	Glu	Arg	Asn	Gly			
					405					410							

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 2301 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

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(ix) FEATURE:

- (A) NAME/KEY: CDS
 (B) LOCATION: 308..1435

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

CTGAGCTGCC GTTACATTCA GGAGAAACAG CAGTGTCCGC GGCTCCCAAT CTCAGAGGGA 60
 ACCTAGGGTA CTGGGGGAGA TGGTGTCCAGG GACATGGACG CCAACCCCCA AGGGTTTCTG 120
 20 CTGCTGGCTA CTCTTCTCTC CAGGCTCTAC TTCTGTTTCAT ACGGTCCATA TCTCCTAGGG 180
 GACCCTGAAA GCCTAGGAAC CGACTCTGGC CATCCATCTC TCCGGAAGA TTATAACCCA 240
 25 GAGTGCTTCT CAGGGGGGAA GAATTTGAAG CAAAACCAGA CCCCAGGGA TCCCCGCTGC 300
 GGCCGCC ATG GCG CAG GAG AAC GCC GCT TTC TCT CCC GGG TCG GAG GAG 349
 Met Ala Gln Glu Asn Ala Ala Phe Ser Pro Gly Ser Glu Glu
 1 5 10
 30 CCG CCA CGC CGC CGC GGT CGC CAG CGC TAC GTG GAG AAG GAC GGT CGC 397
 Pro Pro Arg Arg Arg Gly Arg Gln Arg Tyr Val Glu Lys Asp Gly Arg
 15 20 25 30
 35 TGT AAC GTG CAG CAG GGC AAC GTC CGC GAG ACC TAC CGC TAC CTG ACC 445
 Cys Asn Val Gln Gln Gly Asn Val Arg Glu Thr Tyr Arg Tyr Leu Thr
 35 40 45
 GAC CTG TTC ACC ACG CTG GTG GAC CTG CAG TGG CGC CTC AGA CTG CTC 493
 40 Asp Leu Phe Thr Thr Leu Val Asp Leu Gln Trp Arg Leu Arg Leu Leu
 50 55 60
 TTC TTC GTG CTC GCC TAC GCG CTC ACT TGG CTC TTC TTC GGT GTC ATC 541
 Phe Phe Val Leu Ala Tyr Ala Leu Thr Trp Leu Phe Phe Gly Val Ile
 45 65 70 75
 TGG TGG CTC ATC GCC TAC GGT CGC GGC GAC CTG GAG CAC CTG GAG GAC 589
 Trp Trp Leu Ile Ala Tyr Gly Arg Gly Asp Leu Glu His Leu Glu Asp
 80 85 90
 50 ACC GCG TGG ACC CCG TGC GTC AAC AAC CTC AAC GGC TTC GTG GCC GCC 637
 Thr Ala Trp Thr Pro Cys Val Asn Asn Leu Asn Gly Phe Val Ala Ala
 95 100 105 110

55

	TTC	CTC	TTC	TCC	ATC	GAG	ACG	GAG	ACC	ACC	ATC	GGC	TAT	GGG	CAC	CGC	685
	Phe	Leu	Phe	Ser	Ile	Glu	Thr	Glu	Thr	Thr	Ile	Gly	Tyr	Gly	His	Arg	
					115					120					125		
5	GTC	ATC	ACC	GAC	CAG	TGT	CCC	GAG	GGC	ATC	GTG	CTG	CTG	CTG	CTG	CAG	733
	Val	Ile	Thr	Asp	Gln	Cys	Pro	Glu	Gly	Ile	Val	Leu	Leu	Leu	Leu	Gln	
				130					135					140			
10	GCT	ATC	CTG	GGC	TCC	ATG	GTG	AAC	GCT	TTC	ATG	GTG	GGC	TGC	ATG	TTC	781
	Ala	Ile	Leu	Gly	Ser	Met	Val	Asn	Ala	Phe	Met	Val	Gly	Cys	Met	Phe	
			145					150					155				
15	GTC	AAG	ATC	TCG	CAG	CCC	AAC	AAG	CGC	GCC	GCC	ACT	CTC	GTC	TTC	TCC	829
	Val	Lys	Ile	Ser	Gln	Pro	Asn	Lys	Arg	Ala	Ala	Thr	Leu	Val	Phe	Ser	
		160					165					170					
20	TCG	CAC	GCC	GTG	GTG	TCT	CTG	CGC	GAC	GGG	CGC	CTC	TGT	CTC	ATG	TTT	877
	Ser	His	Ala	Val	Val	Ser	Leu	Arg	Asp	Gly	Arg	Leu	Cys	Leu	Met	Phe	
	175					180					185					190	
	CGC	GTG	GGC	GAC	CTG	CGA	TCC	TCA	CAC	ATC	GTC	GAG	GCC	TCC	ATC	CGA	925
	Arg	Val	Gly	Asp	Leu	Arg	Ser	Ser	His	Ile	Val	Glu	Ala	Ser	Ile	Arg	
				195						200					205		
25	GCC	AAG	CTC	ATC	CGC	TCC	CGT	CAG	ACG	CTC	GAG	GGC	GAG	TTC	ATC	CCT	973
	Ala	Lys	Leu	Ile	Arg	Ser	Arg	Gln	Thr	Leu	Glu	Gly	Glu	Phe	Ile	Pro	
				210					215					220			
30	TTG	CAC	CAG	ACC	GAC	CTC	AGC	GTG	GGC	TTT	GAC	ACG	GGG	GAC	GAC	CGC	1021
	Leu	His	Gln	Thr	Asp	Leu	Ser	Val	Gly	Phe	Asp	Thr	Gly	Asp	Asp	Arg	
			225					230					235				
35	CTC	TTT	CTC	GTC	TCA	CCT	CTC	GTC	ATC	AGC	CAC	GAA	ATC	GAT	GCC	GCC	1069
	Leu	Phe	Leu	Val	Ser	Pro	Leu	Val	Ile	Ser	His	Glu	Ile	Asp	Ala	Ala	
		240					245					250					
40	AGC	CCC	TTC	TGG	GAG	GCA	TCG	CGC	CGC	GCC	CTC	GAG	AGG	GAC	GAC	TTC	1117
	Ser	Pro	Phe	Trp	Glu	Ala	Ser	Arg	Arg	Ala	Leu	Glu	Arg	Asp	Asp	Phe	
	255					260					265					270	
	GAG	ATC	GTA	GTC	ATT	CTC	GAG	GGC	ATG	GTG	GAG	GCC	ACG	GGA	ATG	ACG	1165
	Glu	Ile	Val	Val	Ile	Leu	Glu	Gly	Met	Val	Glu	Ala	Thr	Gly	Met	Thr	
				275					280						285		
45	TGC	CAA	GCT	CGA	AGC	TCG	TAC	CTG	GTG	GAT	GAA	GTG	TTG	TGG	GGA	CAC	1213
	Cys	Gln	Ala	Arg	Ser	Ser	Tyr	Leu	Val	Asp	Glu	Val	Leu	Trp	Gly	His	
				290					295					300			
50	CGG	TTC	ACA	TCC	GTG	CTC	ACC	CTG	GAG	GAT	GGT	TTC	TAT	GAG	GTG	GAC	1261
	Arg	Phe	Thr	Ser	Val	Leu	Thr	Leu	Glu	Asp	Gly	Phe	Tyr	Glu	Val	Asp	
			305					310					315				
55	TAC	GCC	AGC	TTC	CAC	GAA	ACC	TTT	GAG	GTG	CCC	ACA	CCC	TCG	TGC	AGT	1309
	Tyr	Ala	Ser	Phe	His	Glu	Thr	Phe	Glu	Val	Pro	Thr	Pro	Ser	Cys	Ser	
		320					325					330					

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55 Met Ala Gln Glu Asn Ala Ala Phe Ser Pro Gly Ser Glu Glu Pro Pro
1 5 10 15

	Arg	Arg	Arg	Gly	Arg	Gln	Arg	Tyr	Val	Glu	Lys	Asp	Gly	Arg	Cys	Asn	
				20					25					30			
5	Val	Gln	Gln	Gly	Asn	Val	Arg	Glu	Thr	Tyr	Arg	Tyr	Leu	Thr	Asp	Leu	
		35						40					45				
	Phe	Thr	Thr	Leu	Val	Asp	Leu	Gln	Trp	Arg	Leu	Arg	Leu	Leu	Phe	Phe	
		50					55					60					
10	Val	Leu	Ala	Tyr	Ala	Leu	Thr	Trp	Leu	Phe	Phe	Gly	Val	Ile	Trp	Trp	
	65					70					75					80	
	Leu	Ile	Ala	Tyr	Gly	Arg	Gly	Asp	Leu	Glu	His	Leu	Glu	Asp	Thr	Ala	
					85					90					95		
15	Trp	Thr	Pro	Cys	Val	Asn	Asn	Leu	Asn	Gly	Phe	Val	Ala	Ala	Phe	Leu	
				100					105					110			
	Phe	Ser	Ile	Glu	Thr	Glu	Thr	Thr	Ile	Gly	Tyr	Gly	His	Arg	Val	Ile	
20			115					120					125				
	Thr	Asp	Gln	Cys	Pro	Glu	Gly	Ile	Val	Leu	Leu	Leu	Leu	Gln	Ala	Ile	
		130					135					140					
25	Leu	Gly	Ser	Met	Val	Asn	Ala	Phe	Met	Val	Gly	Cys	Met	Phe	Val	Lys	
	145					150					155					160	
	Ile	Ser	Gln	Pro	Asn	Lys	Arg	Ala	Ala	Thr	Leu	Val	Phe	Ser	Ser	His	
					165					170					175		
30	Ala	Val	Val	Ser	Leu	Arg	Asp	Gly	Arg	Leu	Cys	Leu	Met	Phe	Arg	Val	
				180					185					190			
	Gly	Asp	Leu	Arg	Ser	Ser	His	Ile	Val	Glu	Ala	Ser	Ile	Arg	Ala	Lys	
35			195					200					205				
	Leu	Ile	Arg	Ser	Arg	Gln	Thr	Leu	Glu	Gly	Glu	Phe	Ile	Pro	Leu	His	
		210					215					220					
40	Gln	Thr	Asp	Leu	Ser	Val	Gly	Phe	Asp	Thr	Gly	Asp	Asp	Arg	Leu	Phe	
	225					230					235					240	
	Leu	Val	Ser	Pro	Leu	Val	Ile	Ser	His	Glu	Ile	Asp	Ala	Ala	Ser	Pro	
					245					250					255		
45	Phe	Trp	Glu	Ala	Ser	Arg	Arg	Ala	Leu	Glu	Arg	Asp	Asp	Phe	Glu	Ile	
				260					265					270			
	Val	Val	Ile	Leu	Glu	Gly	Met	Val	Glu	Ala	Thr	Gly	Met	Thr	Cys	Gln	
50			275					280					285				
	Ala	Arg	Ser	Ser	Tyr	Leu	Val	Asp	Glu	Val	Leu	Trp	Gly	His	Arg	Phe	
		290					295					300					
55	Thr	Ser	Val	Leu	Thr	Leu	Glu	Asp	Gly	Phe	Tyr	Glu	Val	Asp	Tyr	Ala	
	305					310					315					320	

